

Swope, Sheridan

From: Swope, Sheridan
Sent: Thursday, June 23, 2005 10:04 AM
To: Schulwitz, Paul
Subject: RE: 10/820,536

Paul,

Please Align SID 47 with any hits that have greater than 90% homology with SID 46.

This includes seqs that have 100% homology.

Thanks,
Sheridan

Noart

-----Original Message-----

From: Schulwitz, Paul
Sent: Thursday, June 23, 2005 8:23 AM
To: Swope, Sheridan
Subject: RE: 10/820,536

As far as I could tell there were no results that were in the range of 90 to 99+%.
There were results that were exactly 100% matches.
I did not feel that there was a reason to align those hits because they are exact matches.
I hope this answers your question.

Paul

-----Original Message-----

From: Swope, Sheridan
Sent: Wednesday, June 22, 2005 3:54 PM
To: Schulwitz, Paul
Subject: FW: 10/820,536

Paul, I received the results from this request.
I see where the NT data bases have been searched for SID 46.
But I don't see in the results where point (2) below has been done.
Please clarify the status of the search.
Thanks,
Sheridan

-----Original Message-----

From: Swope, Sheridan
Sent: Thursday, June 09, 2005 6:36 PM
To: STIC-Biotech/ChemLib
Cc: O'Bryen, Barbara
Subject: 10/820,536

For 10/820,536, pls search and interference search the following.

- (1) SID 46 against the NT data bases
- (2) Align SID 47 with any hits from (1) that have greater than 90% homology



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 156051

TO: Sheridan Swope
Location: REM-2B71/2C70
Art Unit: 1652
Monday, June 2005

Case Serial Number: 10/820536

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: 571-272-2527

Paul.schulwitz@uspto.gov

Search Notes

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 10:59:17 ; Search time 0.001 Seconds
(without alignments)
3.362 Million cell updates/sec

Title: us-10-820-536-47
Perfect score: 41
Sequence: 1 cctagtcgactattctcc.....ttgaataatgctttatc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 segs, 41 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : ar271714.gb_pat:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 9.8 | 23.9 | 41 | 1 AR271714 | ACCESSION:AR271714 |
| 2 | 8.4 | 20.5 | 41 | 1 AR271714 | ACCESSION:AR271714 |

ALIGNMENTS

RESULT 1
AR271714
LOCUS AR271714 41 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 32 from patent US 6503744.
ACCESSION AR271714
VERSION AR271714.1 GI:29703259
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 41)
AUTHORS Gilbert,M. and Makarchuk,W.W.
TITLE Campylobacter glycosyltransferases for biosynthesis of gangliosides
and ganglioside mimics
JOURNAL Patent: US 6503744-A 32 07-JAN-2003;
FEATURES
source
Location/Qualifiers
1..41
/organism="unknown"
/mol_type="genomic DNA"

Query Match 23.9%; Score 9.8; DB 1; Length 41;

Best Local Similarity 66.7%; Pred. No. 0;
Matches 14; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

0Y 18 TCCTTGAATAATGCTTAT 38
||| ||||| |||

DB 10 TCATATGAAAAAGTTATAT 30

RESULT 2
AR271714/c
LOCUS AR271714 41 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 32 from patent US 6503744.
ACCESSION AR271714
VERSION AR271714.1 GI:29703259
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 41)
AUTHORS Gilbert,M. and Makarchuk,W.W.
TITLE Campylobacter glycosyltransferases for biosynthesis of gangliosides
and ganglioside mimics
JOURNAL Patent: US 6503744-A 32 07-JAN-2003;
FEATURES
source
1..41
/organism="unknown"
/mol_type="genomic DNA"

Query Match 20.5%; Score 8.4; DB 1; Length 41;
Best Local Similarity 66.7%; Pred. No. 0;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

0Y 24 GAATATGCTTATATC 41
||| ||||| |||
DB 33 GCAATAATACCTTTTC 16

Search completed: June 23, 2005, 10:59:17
Job time : 0.001 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 11:01:37 ; Search time 0.001 Seconds
(without alignments)
3.362 Million cell updates/sec

Title: us-10-820-536-47

Perfect score: 41
Sequence: 1 cctagcgcgactatttcc.....ttgaataatgcttatatc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 segs, 41 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : us-10-820-536-46:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------|
| 1 | 9.8 | 23.9 | 41 | 1 | us-10-820-536-46 |
| 2 | 8.4 | 20.5 | 41 | 1 | us-10-820-536-46 |

ALIGNMENTS

RESULT 1
us-10-820-536-46

Query Match 23.9%; Score 9.8; DB 1; Length 41;
Best Local Similarity 66.7%; Pred. No. 0;
Matches 14; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 18 TCCTTGAATTAAGCTTTAT 38
DB 10 TCATATGAAAAAGTTATTAT 30

RESULT 2
us-10-820-536-46/c

Query Match 20.5%; Score 8.4; DB 1; Length 41;
Best Local Similarity 66.7%; Pred. No. 0;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 24 GAAATATGCTTATATC 41
DB 33 GCAATATATTAACCTTTTTC 16

Search completed: June 23, 2005, 11:01:37
Job time : 0.001 secs